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## AMENDED CLAIMS

[received by the International Bureau on 26 July 1999 (26.07.99);
original claim 1 amended; original claims 2- 25 cancelled;
new claims 2-88 added; (19 pages)]

What is claimed:

1. An invention substantially as described in the description.

2. An invention substantially as described and illustrated in the description.

3. A process for identifying one or more bi-allelic markers linked to a bi-allelic genetic characteristic gene in a species of creatures, comprising the steps of :

a)choosing two or more bi-allelic covering markers so that a CL-F region is systematically covered by the two or more covering markers, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency;

b)choosing a statistical linkage test based on allelic association for each covering marker;

c)choosing a sample of individuals for each covering marker ;

d)obtaining genotype data/sample allele frequency data for each covering marker and the sample chosen for each covering marker, and obtaining phenotype status data for the genetic characteristic for each individual in the sample chosen for each covering marker;

e)calculating evidence for linkage between each covering marker and the gene using the statistical linkage test based on allelic association chosen for each covering marker and the genotype data/sample allele frequency data for each covering marker and using the phenotype status data for the genetic characteristic for each individual in the sample chosen for each covering marker obtained in d); and

f)identifying those covering markers as linked to the genetic characteristic gene which show evidence for linkage based on the calculations of step e.

4. A process as in claim 3, wherein the CL-F region is N covered to within a CL-F distance $\delta$ by the two or more bi-allelic covering markers, so that each point in the region is within the CL-F distance $\delta$ of N or more of the covering markers, wherein $\delta$ is equal to about [ $\delta_{CL}$, 0.25] or the equivalent thereof, $\delta_{CL}$ is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1.

5. A process as in claim 4, wherein the CL-F region comprises a CL-F matrix, the sum of the number of columns and rows in the matrix being greater than or equal to three, each cell of the matrix being of length $L_{MC}$ and width $W_{MC}$, and $L_{MC}$ being less than or equal to about $\delta_{CL}$, and $W_{MC}$ being less than or equal to about 0.25, $\delta_{CL}$ is equal to the largest chromosomal length, computed by any method, for which

linkage disequilibrium has been observed between any polymorphisms in any population of the species, there being N or more covering markers in each cell of the matrix and N is an integer greater than or equal to 1.

6. A process as in claim 5, wherein the covering markers are substantially nonevenly distributed across a chromosome or a chromosomal segment.

7. A process as in claim 5, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein the least common allele frequency of one or more markers is less than 0.4.

8. A process as in claim 5, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment; and wherein there is a subgroup of one or more of the covering markers, and each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

9. A process as in claim 5, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein (1) the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof and the least common allele frequency of one or more of the covering markers is less than 0.3 or wherein (2) the least common allele frequency of one or more of the covering markers is less than 0.2.

10. A process as in claim 5, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof, and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the approximate chromosomal distribution of the covering markers, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

11. A process as in claim 5, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the approximate chromosomal distribution of the covering markers, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

12. A process as in claim 10, wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers

located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the chromosomal distribution of the covering markers on the chromosome segments of the set, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

13. A process as in claim 11, wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the chromosomal distribution of the covering markers on the chromosome segments of the set, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

14. A process as in claim 5, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof, and wherein collection C is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection C if and only if the group substantially meets criteria (1), (2), (3) and (4): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive, (2) the number of markers in the group is the same as the number of covering markers, (3) the chromosomal distribution of the group of markers and the covering markers is substantially similar, and (4) the marker type of each group marker and the covering marker with substantially the same chromosomal location is the same; wherein a group that is a member of collection C substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection C that meet criterion (5); wherein P is less than about 90 percent.

15. A process as in claim 5, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof, and wherein collection C is essentially the collection of known groups of bi-allelic markers with least common allele frequencies

between 0.3 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection C if and only if the group substantially meets criteria (1), (2), (3) and (4): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive, (2) the number of markers in the group is the same as the number of covering markers, (3) the chromosomal distribution of the group of markers and the covering markers is substantially similar, and (4) the marker type of each group marker and the covering marker with substantially the same chromosomal location is the same; wherein a group that is a member of collection C substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection C that meet criterion (5); wherein P is less than about 90 percent.

16. A process as in claim 5, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof; wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; wherein collection D is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection D if and only if the group substantially meets criteria (1), (2), and (3): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive, (2) the number of covering markers and the number of group markers located on each chromosome segment of the set is the same, and (3) there is a group marker of the same type as each covering marker located on the same chromosome segment of the set as each covering marker; wherein a group that is a member of collection D substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection D that meet criterion (5); wherein P is less than about 90 percent.

17. A process as in claim 5, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof; wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set,

and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; wherein collection D is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection D if and only if the group substantially meets criteria (1), (2), and (3): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive, (2) the number of covering markers and the number of group markers located on each chromosome segment of the set is the same, and (3) there is a group marker of the same type as each covering marker located on the same chromosome segment of the set as each covering marker; wherein a group that is a member of collection D substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection D that meet criterion (5); wherein P is less than about 90 percent.

18. A process as in claim 4, wherein $\delta$ is less than or equal to about [1 cM, 0.15] or the equivalent thereof.

19. A process as in claim 4, wherein (1) the covering markers are substantially nonevenly distributed across a chromosome or a chromosomal segment or (2) wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein the least common allele frequency of one or more markers is less than 0.4 or (3) wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment; and wherein there is a subgroup of one or more of the covering markers, and each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

20. A process as in any one of claims 3-19, wherein there is a group of covering markers, and the markers in the group are a majority of the covering markers, and each marker in the group is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

21. A process as in claim 5 wherein $L_{MC}$ is less than or equal to about 250,000 bp or the equivalent thereof, $W_{MC}$ is less than or equal to about 0.15, wherein the species is human being, wherein the same statistical linkage test based on allelic association is chosen for each covering marker in step b) and wherein there is a group of covering markers, and the markers in the group are a majority of the covering markers, and each marker in the group is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

22. An apparatus for identifying bi-allelic markers linked to a bi-allelic genetic characteristic gene in a species of creatures, comprising: means to practice each of the steps of a process as in any one of the claims 3-21.

23. A process as in any one of claims 3-21, wherein the process comprises a computer program.

24. An apparatus as in claim 22, wherein the apparatus comprises a computer, the computer being supplied with proper data and instructions.

25. A process for localizing a bi-alleic genetic characteristic gene in a species of creatures to a CL-F location, comprising the steps of: any one of the processes in claims 3-21; further comprising: the step f) localizing the gene to the CL-F location of one or more markers that show evidence for linkage based on the calculations of step e).

26. A process as in claim 25, wherein the process comprises a computer program.

27. An apparatus for localizing a bi-alleic genetic characteristic gene in a species of creatures to a CL-F location, comprising: means to practice each of the steps of a process as in claim 25.

28. An apparatus for localizing a bi-alleic genetic characteristic gene in a species of creatures to a CL-F location as in claim 27, wherein the apparatus comprises a computer, the computer being supplied with proper data and instructions.

29. A process for obtaining genotype data/sample allele frequency data for each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals of a sample, each individual in the sample being a member of the same species, comprising:

a)determining information on the presence or absence of each allele of each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals of a sample, a CL-F region being systematically covered by the two or more bi-allelic covering markers, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency; and

b) transforming the information of step a) into genotype data/sample allele frequency data for each marker of the group.

30. A process for obtaining genotype data/sample allele frequency data as in claim 29, wherein the CL-F region is N covered to within a CL-F distance $\delta$ by the two or more bi-allelic covering markers, so that each point in the region is within the CL-F distance $\delta$ of N or more of the covering markers, wherein $\delta$ is equal to about [ $\delta_{CL}$, 0.25] or the equivalent thereof, $\delta_{CL}$ is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1.

31. A process for obtaining genotype data/sample allele frequency data as in claim 30, wherein the CL-F region comprises a CL-F matrix, the sum of the number of columns and rows in the matrix being greater than or equal to three, each cell of the matrix being of length $L_{MC}$ and width $W_{MC}$, and $L_{MC}$ being less than or equal to about $\delta_{CL}$, and $W_{MC}$ being less than or equal to about 0.25, $\delta_{CL}$ is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, there being N or more covering markers in each cell of the matrix and N is an integer greater than or equal to 1.

32. A process for obtaining genotype data/sample allele frequency data as in claim 31, wherein the covering markers are substantially nonevenly distributed across a chromosome or a chromosomal segment.

33. A process for obtaining genotype data/sample allele frequency data as in claim 31, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein the least common allele frequency of one or more markers is less than 0.4.

34. A process for obtaining genotype data/sample allele frequency data as in claim 31, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment; and wherein there is a subgroup of one or more of the covering markers, and each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

35. A process for obtaining genotype data/sample allele frequency data as in claim 31, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein (1) the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof and the least common allele frequency of one or more of the covering markers is less than 0.3 or wherein (2) the least common allele frequency of one or more of the covering markers is less than 0.2.

36. A process for obtaining genotype data/sample allele frequency data as in claim 31, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof, and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the approximate chromosomal distribution of the covering markers, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

37. A process for obtaining genotype data/sample allele frequency data as in claim 31, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the approximate chromosomal distribution of the covering markers, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

38. A process for obtaining genotype data/sample allele frequency data as in claim 36, wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the

set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the chromosomal distribution of the covering markers on the chromosome segments of the set, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

39. A process for obtaining genotype data/sample allele frequency data as in claim 37, wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the chromosomal distribution of the covering markers on the chromosome segments of the set, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

40. A process for obtaining genotype data/sample allele frequency data as in claim 31, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof, and wherein collection C is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection C if and only if the group substantially meets criteria (1), (2), (3) and (4): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive, (2) the number of markers in the group is the same as the number of covering markers, (3) the chromosomal distribution of the group of markers and the covering markers is substantially similar, and (4) the marker type of each group marker and the covering marker with substantially the same chromosomal location is the same; wherein a group that is a member of collection C substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection C that meet criterion (5); wherein P is less than about 90 percent.

41. A process for obtaining genotype data/sample allele frequency data as in claim 31, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal

segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof, and wherein collection C is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection C if and only if the group substantially meets criteria (1), (2), (3) and (4): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive, (2) the number of markers in the group is the same as the number of covering markers, (3) the chromosomal distribution of the group of markers and the covering markers is substantially similar, and (4) the marker type of each group marker and the covering marker with substantially the same chromosomal location is the same; wherein a group that is a member of collection C substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection C that meet criterion (5); wherein P is less than about 90 percent.

42. A process for obtaining genotype data/sample allele frequency data as in claim 31, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof; wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; wherein collection D is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection D if and only if the group substantially meets criteria (1), (2), and (3): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive, (2) the number of covering markers and the number of group markers located on each chromosome segment of the set is the same, and (3) there is a group marker of the same type as each covering marker located on the same chromosome segment of the set as each covering marker; wherein a group that is a member of collection D substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection D that meet criterion (5); wherein P is less than about 90 percent.

43. A process for obtaining genotype data/sample allele frequency data as in claim 31, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof; wherein the chromosome or the chromosomal segment consists

essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; wherein collection D is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection D if and only if the group substantially meets criteria (1), (2), and (3): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive, (2) the number of covering markers and the number of group markers located on each chromosome segment of the set is the same, and (3) there is a group marker of the same type as each covering marker located on the same chromosome segment of the set as each covering marker; wherein a group that is a member of collection D substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection D that meet criterion (5); wherein P is less than about 90 percent.

44. A process for obtaining genotype data/sample allele frequency data as in claim 30, wherein $\delta$ is less than or equal to about [1 cM, 0.15] or the equivalent thereof.

45. A process for obtaining genotype data/sample allele frequency data as in claim 30, wherein (1) the covering markers are substantially nonevenly distributed across a chromosome or a chromosomal segment or (2) wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein the least common allele frequency of one or more markers is less than 0.4 or (3) wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment; and wherein there is a subgroup of one or more of the covering markers, and each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

46. A process for obtaining genotype data/sample allele frequency data as in any one of claims 29-45, wherein there is a group of covering markers, and the markers in the group are a majority of the covering markers, and each marker in the group is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

47. A process for obtaining genotype data/sample allele frequency data as in claim 31 wherein $L_{MC}$ is less than or equal to about 250,000 bp or the equivalent thereof, $W_{MC}$ is less than or equal to about 0.15, wherein the species is human being, wherein the same statistical linkage test based on allelic association is chosen for each covering marker in step b) and wherein there is a group of covering markers, and the markers in the group are a majority of the covering markers, and each marker in the group is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

48. An apparatus for obtaining genotype data/sample allele frequency data for each bi-allelic marker of a group of two or more bi-allelic covering markers in the chromosomal DNA of one or more individuals of a sample, each individual in the sample being a member of the same species, comprising: means to practice each of the steps of a process as in any one of the claims 29-47.

49. A process for obtaining genotype data/sample allele frequency data as in any one of claims 29-47, wherein the process comprises a computer program.

50. An apparatus as in claim 48, wherein the apparatus comprises a computer, the computer being supplied with proper data and instructions.

51. The use of one or more copies of a set of oligonucleotides to determine genotype data/sample allele frequency data for each bi-allelic marker of a group of two or more bi-allelic covering markers for one or more individuals, each individual being a member of the same species, wherein the group of covering markers systematically cover a CL-F region, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency.

52. The use as in claim 51, wherein the CL-F region is N covered to within a CL-F distance $\delta$ by the two or more bi-allelic covering markers, so that each point in the region is within the CL-F distance $\delta$ of N or more of the covering markers, wherein $\delta$ is equal to about [ $\delta_{CL}$, 0.25] or the equivalent thereof, $\delta_{CL}$ is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1.

53. The use as in claim 51, wherein the CL-F region comprises a CL-F matrix, the sum of the number of columns and rows in the matrix being greater than or equal to three, each cell of the matrix being of length $L_{MC}$ and width $W_{MC}$, and $L_{MC}$ being less than or equal to about $\delta_{CL}$, and $W_{MC}$ being less than or equal to about 0.25, $\delta_{CL}$ is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, there being N or more covering markers in each cell of the matrix and N is an integer greater than or equal to 1.

54. The use as in claim 53, wherein the covering markers are substantially nonevenly distributed across a chromosome or a chromosomal segment.

55. The use as in claim 53, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein the least common allele frequency of one or more markers is less than 0.4.

56. The use as in claim 53, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment; and wherein there is a subgroup of one or more of the covering markers, and each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

57. The use as in claim 53, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein (1) the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof and the least common allele

frequency of one or more of the covering markers is less than 0.3 or wherein (2) the least common allele frequency of one or more of the covering markers is less than 0.2.

58. The use as in claim 53, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof, and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the approximate chromosomal distribution of the covering markers, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

59. The use as in claim 53, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the approximate chromosomal distribution of the covering markers, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

60. The use as in claim 58, wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the chromosomal distribution of the covering markers on the chromosome segments of the set, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

61. The use as in claim 59, wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; and

wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the chromosomal distribution of the covering markers on the chromosome segments of the set, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

62. The use as in claim 53, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof, and wherein collection C is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection C if and only if the group substantially meets criteria (1), (2), (3) and (4): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive, (2) the number of markers in the group is the same as the number of covering markers, (3) the chromosomal distribution of the group of markers and the covering markers is substantially similar, and (4) the marker type of each group marker and the covering marker with substantially the same chromosomal location is the same; wherein a group that is a member of collection C substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection C that meet criterion (5); wherein P is less than about 90 percent.

63. The use as in claim 53, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof, and wherein collection C is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection C if and only if the group substantially meets criteria (1), (2), (3) and (4): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive, (2) the number of markers in the group is the same as the number of covering markers, (3) the chromosomal distribution of the group of markers and the covering markers is substantially similar, and (4) the marker type of each group marker and the covering marker with substantially the same chromosomal location is the same; wherein a group that is a member of collection C substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection C that meet criterion (5); wherein P is less than about 90 percent.

64. The use as in claim 53, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof; wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of

substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; wherein collection D is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection D if and only if the group substantially meets criteria (1), (2), and (3): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive, (2) the number of covering markers and the number of group markers located on each chromosome segment of the set is the same, and (3) there is a group marker of the same type as each covering marker located on the same chromosome segment of the set as each covering marker; wherein a group that is a member of collection D substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection D that meet criterion (5); wherein P is less than about 90 percent.

65. The use as in claim 53, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof; wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; wherein collection D is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection D if and only if the group substantially meets criteria (1), (2), and (3): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive, (2) the number of covering markers and the number of group markers located on each chromosome segment of the set is the same, and (3) there is a group marker of the same type as each covering marker located on the same chromosome segment of the set as each covering marker; wherein a group that is a member of collection D substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection D that meet criterion (5); wherein P is less than about 90 percent.

66. The use as in claim 52, wherein $\delta$ is less than or equal to about [1 cM, 0.15] or the equivalent thereof.

67. The use as in claim 52, wherein (1) the covering markers are substantially nonevenly distributed across a chromosome or a chromosomal segment or (2) wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein the least common allele frequency of one or more markers is less than 0.4 or (3) wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment; and wherein there is a subgroup of one or more of the covering markers, and each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

68. The use as in any one of claims 51-67, wherein there is a group of covering markers, and the markers in the group are a majority of the covering markers, and each marker in the group is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

69. The use as in claim 53 wherein $L_{MC}$ is less than or equal to about 250,000 bp or the equivalent thereof, $W_{MC}$ is less than or equal to about 0.15, wherein the species is human being, wherein the same statistical linkage test based on allelic association is chosen for each covering marker in step b) and wherein there is a group of covering markers, and the markers in the group are a majority of the covering markers, and each marker in the group is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

70. One or more copies of a set of oligonucleotides, the set of oligonucleotides being complementary to a group of two or more bi-allelic covering markers of the same species, wherein the group of covering markers systematically cover a CL-F region, the CL-F region being a collection of points on a two-dimensional plane, the two-dimensional plane having the two orthogonal dimensions of chromosomal location and least common allele frequency.

71. One or more copies of a set of oligonucleotides as in claim 70, wherein the CL-F region is N covered to within a CL-F distance $\delta$ by the two or more bi-allelic covering markers, so that each point in the region is within the CL-F distance $\delta$ of N or more of the covering markers, wherein $\delta$ is equal to about [ $\delta_{CL}$, 0.25] or the equivalent thereof, $\delta_{CL}$ is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, N is an integer greater than or equal to 1.

72. One or more copies of a set of oligonucleotides as in claim 70, wherein the CL-F region comprises a CL-F matrix, the sum of the number of columns and rows in the matrix being greater than or equal to three, each cell of the matrix being of length $L_{MC}$ and width $W_{MC}$, and $L_{MC}$ being less than or equal to about $\delta_{CL}$, and $W_{MC}$ being less than or equal to about 0.25, $\delta_{CL}$ is equal to the largest chromosomal length, computed by any method, for which linkage disequilibrium has been observed between any polymorphisms in any population of the species, there being N or more covering markers in each cell of the matrix and N is an integer greater than or equal to 1.

73. One or more copies of a set of oligonucleotides as in claim 72, wherein the covering markers are substantially nonevenly distributed across a chromosome or a chromosomal segment.

74. One or more copies of a set of oligonucleotides as in claim 72, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein the least common allele frequency of one or more markers is less than 0.4.

75. One or more copies of a set of oligonucleotides as in claim 72, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment; and wherein there is a subgroup of one or more of the covering markers, and each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

76. One or more copies of a set of oligonucleotides as in claim 72, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein (1) the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof and the least common allele frequency of one or more of the covering markers is less than 0.3 or wherein (2) the least common allele frequency of one or more of the covering markers is less than 0.2.

77. One or more copies of a set of oligonucleotides as in claim 72, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof, and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the approximate chromosomal distribution of the covering markers, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

78. One or more copies of a set of oligonucleotides as in claim 72, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the approximate chromosomal distribution of the covering markers, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

79. One or more copies of a set of oligonucleotides as in claim 77, wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome

segments with one or zero covering markers located thereon; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the chromosomal distribution of the covering markers on the chromosome segments of the set, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

80. One or more copies of a set of oligonucleotides as in claim 78, wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; and wherein the conditional probability the covering markers were chosen essentially randomly from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive is less than about 10 percent; wherein the conditional probability is substantially conditional on (1) the chromosomal distribution of the covering markers on the chromosome segments of the set, (2) the marker type of each covering marker and (3) there being N or more covering markers in each cell of the matrix.

81. One or more copies of a set of oligonucleotides as in claim 72, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof, and wherein collection C is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection C if and only if the group substantially meets criteria (1), (2), (3) and (4): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive, (2) the number of markers in the group is the same as the number of covering markers, (3) the chromosomal distribution of the group of markers and the covering markers is substantially similar, and (4) the marker type of each group marker and the covering marker with substantially the same chromosomal location is the same; wherein a group that is a member of collection C substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection C that meet criterion (5); wherein P is less than about 90 percent.

82. One or more copies of a set of oligonucleotides as in claim 72, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof, and wherein collection C is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive that are substantially similar to

the covering markers as a group; wherein a group of bi-allelic markers is a member of collection C if and only if the group substantially meets criteria (1), (2), (3) and (4): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive, (2) the number of markers in the group is the same as the number of covering markers, (3) the chromosomal distribution of the group of markers and the covering markers is substantially similar, and (4) the marker type of each group marker and the covering marker with substantially the same chromosomal location is the same; wherein a group that is a member of collection C substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection C that meet criterion (5); wherein P is less than about 90 percent.

83. One or more copies of a set of oligonucleotides as in claim 72, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is less than or equal to 2 cM or the equivalent thereof; wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; wherein collection D is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection D if and only if the group substantially meets criteria (1), (2), and (3): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.2 inclusive and 0.5 inclusive, (2) the number of covering markers and the number of group markers located on each chromosome segment of the set is the same, and (3) there is a group marker of the same type as each covering marker located on the same chromosome segment of the set as each covering marker; wherein a group that is a member of collection D substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection D that meet criterion (5); wherein P is less than about 90 percent.

84. One or more copies of a set of oligonucleotides as in claim 72, wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, wherein the average chromosomal intermarker distance of the covering markers is greater than 2 cM or the equivalent thereof; wherein the chromosome or the chromosomal segment consists essentially of a set of nonoverlapping chromosome segments of substantially equal length, and wherein one and only one covering marker is located on each of 80 percent or more of the chromosome segments of the set, and wherein zero or two and only two covering markers are located on each of 20 percent or less of the

chromosome segments of the set, and wherein each chromosome segment with zero covering markers located thereon is bordered only by chromosome segments with one or two covering markers located thereon, and wherein each chromosome segment with two covering markers located thereon is bordered only by chromosome segments with one or zero covering markers located thereon; wherein collection D is essentially the collection of known groups of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive that are substantially similar to the covering markers as a group; wherein a group of bi-allelic markers is a member of collection D if and only if the group substantially meets criteria (1), (2), and (3): (1) each marker in the group is chosen from substantially the known set of bi-allelic markers with least common allele frequencies between 0.3 inclusive and 0.5 inclusive, (2) the number of covering markers and the number of group markers located on each chromosome segment of the set is the same, and (3) there is a group marker of the same type as each covering marker located on the same chromosome segment of the set as each covering marker; wherein a group that is a member of collection D substantially meets criterion (5) if and only if (5) there are N or more of the group markers in each cell of the matrix; wherein P is essentially the proportion of groups in collection D that meet criterion (5); wherein P is less than about 90 percent.

85. One or more copies of a set of oligonucleotides as in claim 71, wherein $\delta$ is less than or equal to about [1 cM, 0.15] or the equivalent thereof.

86. One or more copies of a set of oligonucleotides as in claim 71, wherein (1) the covering markers are substantially nonevenly distributed across a chromosome or a chromosomal segment or (2) wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment, and wherein the least common allele frequency of one or more markers is less than 0.4 or (3) wherein the covering markers are substantially evenly distributed across a chromosome or a chromosomal segment; and wherein there is a subgroup of one or more of the covering markers, and each of the markers in the subgroup is chosen without substantial preference for the least common allele frequency of each of the markers in the subgroup being close to 0.5.

87. One or more copies of a set of oligonucleotides as in any one of claims 70-86, wherein there is a group of covering markers, and the markers in the group are a majority of the covering markers, and each marker in the group is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

88. One or more copies of a set of oligonucleotides as in claim 72 wherein $L_{MC}$ is less than or equal to about 250,000 bp or the equivalent thereof, $W_{MC}$ is less than or equal to about 0.15, wherein the species is human being, wherein the same statistical linkage test based on allelic association is chosen for each covering marker in step b) and wherein there is a group of covering markers, and the markers in the group are a majority of the covering markers, and each marker in the group is an SNP, or a bi-allelic marker equivalent formed only from one or more SNPs.

# Statement under Article 19(1)

Some of the amended claims make use of the phrase "conditional probability", such as claim 11. Some of the amended claims make use of the phrase "proportion of groups", such as claim 14. There are various techniques to calculate or estimate such a probability or such a proportion. These techniques include, but are not necessarily limited to, direct calculation, statistical estimates, and Monte Carlo estimation techniques. Powerful software is available for calculation and statistical estimation for data in matrix format or two-dimensional format. Some such software is available from Cytel Software Corporation, Cambridge, Massachusetts ( example: Exact Logistic Regression: Theory and Examples, Mehta CR, Patel NR, Statistics in Medicine, vol 14, 2143-2160(1995). Another example is SAS (SAS Institute Inc., SAS Campus Drive, Cary, North Carolina 27513, USA.; A handbook of statistical analyses using SAS by Brian S. Everitt and Geoff Der, Boca Raton, Fla. : Chapman & Hall/CRC, 1998.). A further example is MATLAB (The MathWorks, Inc. 3 Apple Hill Drive, Natick, Mass. U.S.A. 01760-2098; MATLAB primer by Kermit Sigmon, 4th ed. Boca Raton : CRC Press, c1994.) Statistical techniques include techniques for hypothesis testing, goodness-of-fit and others.

The degree of skill in the art in probability and statistics is great. Indeed the inventor's important equation (Equation 2, page 38) is an equation for $P_t$, wherein $P_t$ is a binomial probability for parental allele 'transmission' which determines the magnitude of the TDT chi-square statistic. $P_S$ (pages 40-42) is also a binomial probability that determines the magnitude of the ASP test statistic. (see Abstract and Paper: Annals of Human Genetics (1998), 62, 159-179. The abstract is available on the World Wide Web and Internet, including at the journal's website.) Skill in the use of computers in the art is also great (page 25).

Some claims, such as claims 11, 12, 13, 14 and others make use of the phrase "substantially the known set of bi-allelic markers". As pointed out in the description (page 25) information on bi-allelic markers can be gained from sources such as the Whitehead Institute or Marshfield Foundation for Biomedical Research. Similar sources of information on Single Nucleotide Polymorphisms can be obtained from sources given in SNP attack on complex traits, Nature Genetics, volume 20 no. 3, Nov 1998, pp. 217-218.

Some claims, such as claims 11, 12, 13, 14 and others make use of the term "marker type" or similar terminology. As stated in the description, a bi-allelic marker may be an SNP, a microsatellite marker, a bi-allelic marker equivalent formed from one or more true bi-alleic markers. "Marker type" means type of true bi-allelic marker as for example an SNP or a microsatellite; or "marker type" means a bi-allelic marker equivalent of a certain type, such as a bi-allelic marker equivalent formed only from one or more SNPs or a bi-allelic marker equivalent formed only from one or more microsatellites.)